SPECIFICATION AMENDMENTS

Please replace the paragraph beginning on page 9, line13, with the following rewritten paragraph:

Figure 21. Secondary structure and transmembrane prediction for 85P1B3. Panel A. (SEQ ID NO: 729) The secondary structure of 85P1B3 protein was predicted using the HNN - Hierarchical Neural Network method (Guermeur, 1997~~, pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=m[sa_nn.html~~), accessed from the ExPasy molecular biology server ~~(www.expasy.ch/tools/)~~. This method indicates the presence and location of alpha helices (h), extended strands (e), and random coils (c) from the primary protein sequence. The percent of the protein in a given secondary structure is also given. Panel B. Schematic representation of the probability of existence of transmembrane regions of 85P1B3 based on the TMpred algorithm of Hofmann and Stoffel which utilizes TMBASE (K. Hofmann, W. Stoffel. TMBASE - A database of membrane spanning protein segments Biol. Chem. Hoppe-Seyler 374:166, 1993). Stretches of amino acids approximately 17-33 amino acids in length with a value greater than 0 are potential transmembrane helices. This program indicates the presence of one helix in 85P1B3. Panel C. Schematic representation of the probability of the existence of transmembrane regions and the extracellular and intracellular orientation of 85P1B3 based on the algorithm of Sonnhammer, von Heijne, and Krogh (Erik, L.L., *et al.*, A hidden Markov model for predicting transmembrane helices in protein sequences. In Proc. of Sixth Int. Conf. on Intelligent Systems for Molecular Biology, p 175-182 Ed J. Glasgow, *et al.*, Menlo Park, CA: AAAI Press, 1998). This program indicates 85P1B3 to be an intracellular protein without transmembrane domains. These transmembrane prediction results are also summarized in Table XXV.

Please replace Example 3 beginning on page 79, line 28, with the following rewritten example:

Example 3: Chromosomal Localization

Chromosomal localization can implicate genes in disease pathogenesis. Several chromosome mapping approaches are available in the art, including fluorescent *in situ* hybridization (FISH), human/hamster radiation hybrid (RH) panels (Walter *et al.*, 1994; Nature Genetics 7:22; Research Genetics, Huntsville Al), human-rodent somatic cell hybrid panels such as is available from the Coriell Institute (Camden, New Jersey), and genomic viewers utilizing BLAST homologies to sequenced and mapped genomic clones (NCBI, Bethesda, Maryland).

85P1B3 maps to chromosome 15q14, using 85P1B3 sequence and the NCBI BLAST tool~~: (www.ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs)~~.

The chromosomal localization of 85P1B3 was also determined using the GeneBridge4 Human/Hamster radiation hybrid (RH) panel (Walter *et al.*, 1994; Nature Genetics 7:22) (Research Genetics, Huntsville Al).

The following PCR primers were used:

85P1B3.1 5' catgggactctgcatcttaattcc 3' (SEQ ID NO: 732)

85P1B3.2 5' caggttcaggctttattgctgtct 3' (SEQ ID NO: 733)

The resulting 85P1B3 mapping vector for the 93 radiation hybrid panel DNAs (10010001010100010100000000000011010000001210110000101110010000101110001001010110011010110110101), ~~and the mapping program available at the internet address www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl, localize~~ the 85P1B3 gene was localized to chromosome 15q13.2- q14.

Of note, chromosome 15q13.2- q14 is a region implicated in cancers (Tomlinson *et al.*, Gastroenterology 1999 Apr; 116(4):789-95).

Please amend the heading on page 100, line 26 as follows:

Other ~~analoguing~~ analoging strategies

Please amend the heading on page 120, line 1 as follows:

Example 36: 85P1B3 Monoclonal ~~Antibody-mediated~~ Antibody-Mediated Inhibition of Tumors *In Vivo*

Please amend the heading on page 121, line 1 as follows:

Example 37: Induction ~~Of~~ of a Specific CTL Response In Humans

Please replace TABLE XXV on page 170 with the following table:

TABLE XXV: Protein Properties

	Bioinformatic Program	~~URL~~	Outcome
ORF	ORF Finder	~~www.ncbi.nlm.gov/gorf~~	13-702 (includes stop)
Protein Length			229 amino acids
Transmembrane region	TM Pred	~~www.ch.embnet.org/~~	one TM at aa 129-149
	HMMTop	~~www.enzim.hu/hmmtop/~~	one TM at aa 134-158
	Sosui	~~www.genome.ad.jp/SOSui/~~	indicates no TM, soluble protein
	TMHMM	~~www.cbs.dtu.dk/services/TMHMM~~	indicates no TM
Signal Peptide	Signal P	~~www.cbs.dtu.dk/services/SignalP/~~	indicates no signal
pI	pI/MW tool	~~www.expasy.ch/tools/~~	pI 7.02
Molecular weight	pI/MW tool	~~www.expasy.ch/tools/~~	24.69 kDa
Localization	PSORT	~~psort.nibb.ac.jp/~~	Cytoplasmic 65 % Mitochondrial 10%
	PSORT II	~~psort.nibb.ac.jp/~~	Mitochondrial 60.9% Cytoplamic 21.7%

Motifs	Pfam	~~www.sanger.ac.uk/Pfam/~~	no motif detected
	Prints	~~www.biochem.ucl.ac.uk/~~	no significant motif
	Blocks	~~www.blocks.fhcrc.org/~~	Soybean trypsin inhibitor protease family, Cytochrome c
	Prosite	~~www.genome.ad.jp/~~	Cytochrome c family, heme binding signature